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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/841,963

DATE: 12/18/2001

TIME: 16:41:38

Raw Seq.
Listng

Input Set : N:\Crf3\RULE60\09841963.raw

Output Set: N:\CRF3\12182001\I841963.raw

1 <110> APPLICANT: MUSC FOUNDATION FOR RESEARCH DEVELOPMENT
 2 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSIS AND TREATMENT
 3 OF CANCER BASED ON THE TRANSCRIPTION FACTOR ETS2
 4 <130> FILE REFERENCE: 9175-006-228
 5 <140> CURRENT APPLICATION NUMBER: 09/841,963
 6 <141> CURRENT FILING DATE: 2001-04-25
 7 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/27805
 W--> 8 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1999-11-23
 9 <160> NUMBER OF SEQ ID NOS: 34
 10 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 12 <210> SEQ ID NO: 1
 13 <211> LENGTH: 2269
 14 <212> TYPE: DNA
 15 <213> ORGANISM: Homo sapiens
 16 <220> FEATURE:
 17 <221> NAME/KEY: CDS
 18 <222> LOCATION: (292)...(1698)
 19 <400> SEQUENCE: 1

ENTERED

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22	acgagtgcgg tgcgcgtcca gctcagagct cccggagccg cccggccagc gtccggcctc	180
23	cctgatcgta tctggccggc gcctcgccc tgcggccggc cgacccggc agccgcgggc	240
24	gcccggcaccgtcccc accaaggcgc ggcctgccc gcacggcag g atg aat	297
25	Met Asn	
26	1	
27	gat ttc gga atc aag aat atg gac cag gta gcc cct gtc gct aac agt	345
28	Asp Phe Gly Ile Lys Asn Met Asp Gln Val Ala Pro Val Ala Asn Ser	
29	5 10 15	
30	tac aga ggg aca ctc aag cgc cag cca gcc ttt gac acc ttt gat ggg	393
31	Tyr Arg Gly Thr Leu Lys Arg Gln Pro Ala Phe Asp Thr Phe Asp Gly	
32	20 25 30	
33	tcc ctg ttt gct ttt cct tct cta aat gaa gag caa aca ctg caa	441
34	Ser Leu Phe Ala Val Phe Pro Ser Leu Asn Glu Glu Gln Thr Leu Gln	
35	35 40 45 50	
36	gaa gtg cca aca ggc ttg gat tcc att tct cat gac tcc gcc aac tgt	489
37	Glu Val Pro Thr Gly Leu Asp Ser Ile Ser His Asp Ser Ala Asn Cys	
38	55 60 65	
39	gaa ttg cct ttg tta acc ccg tgc agc aag gct gtg atg agt caa gcc	537
40	Glu Leu Pro Leu Leu Thr Pro Cys Ser Lys Ala Val Met Ser Gln Ala	
41	70 75 80	
42	tta aaa gct acc ttc agt ggc ttc aaa aag gaa cag cgg cgc ctg ggc	585
43	Leu Lys Ala Thr Phe Ser Gly Phe Lys Glu Gln Arg Arg Leu Gly	
44	85 90 95	
45	att cca aag aac ccc tgg ctg tgg agt gag caa cag gta tgc cag tgg	633
46	Ile Pro Lys Asn Pro Trp Leu Trp Ser Glu Gln Gln Val Cys Gln Trp	
47	100 105 110	
48	ctt ctc tgg gcc acc aat gag ttc agt ctg gtg aac gtg aat ctg cag	681

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49	Leu	Leu	Trp	Ala	Thr	Asn	Glu	Phe	Ser	Leu	Val	Asn	Val	Asn	Leu	Gln	
50	115					120				125						130	
51	agg	ttc	ggc	atg	aat	ggc	cag	atg	ctg	tgt	aac	ctt	ggc	aag	gaa	cgc	729
52	Arg	Phe	Gly	Met	Asn	Gly	Gln	Met	Leu	Cys	Asn	Leu	Gly	Lys	Glu	Arg	
53						135				140					145		
54	ttt	ctg	gag	ctg	gca	cct	gac	ttt	gtg	ggt	gac	att	ctc	tgg	gaa	cat	777
55	Phe	Leu	Glu	Leu	Ala	Pro	Asp	Phe	Val	Gly	Asp	Ile	Leu	Trp	Glu	His	
56						150				155					160		
57	ctg	gag	caa	atg	atc	aaa	gaa	aac	caa	gaa	aag	aca	gaa	gat	caa	tat	825
58	Leu	Glu	Gln	Met	Ile	Lys	Glu	Asn	Gln	Glu	Lys	Thr	Glu	Asp	Gln	Tyr	
59						165				170					175		
60	gaa	gaa	aat	tca	cac	ctc	acc	tcc	gtt	cct	cat	tgg	att	aac	agc	aat	873
61	Glu	Glu	Asn	Ser	His	Leu	Thr	Ser	Val	Pro	His	Trp	Ile	Asn	Ser	Asn	
62						180				185					190		
63	aca	tta	ggt	ttt	ggc	aca	gag	cag	gcg	ccc	tat	gga	atg	cag	aca	cag	921
64	Thr	Leu	Gly	Phe	Gly	Thr	Glu	Gln	Ala	Pro	Tyr	Gly	Met	Gln	Thr	Gln	
65						195				200					205		210
66	aat	tac	ccc	aaa	ggc	ggc	ctc	ctg	gac	agc	atg	tgt	ccg	gcc	tcc	aca	969
67	Asn	Tyr	Pro	Lys	Gly	Gly	Leu	Leu	Asp	Ser	Met	Cys	Pro	Ala	Ser	Thr	
68						215				220					225		
69	ccc	agc	gta	ctc	agc	tct	gag	cag	gag	ttt	cag	atg	ttc	ccc	aag	tct	1017
70	Pro	Ser	Val	Leu	Ser	Ser	Glu	Gln	Glu	Phe	Gln	Met	Phe	Pro	Lys	Ser	
71						230				235					240		
72	cgg	ctc	agc	tcc	gtc	agc	gtc	acc	tac	tgc	tct	gtc	agt	cag	gac	ttc	1065
73	Arg	Leu	Ser	Ser	Val	Ser	Val	Thr	Tyr	Cys	Ser	Val	Ser	Gln	Asp	Phe	
74						245				250					255		
75	cca	ggc	agc	aac	ttg	aat	ttg	ctc	acc	aac	aat	tct	ggg	act	ccc	aaa	1113
76	Pro	Gly	Ser	Asn	Leu	Asn	Leu	Leu	Thr	Asn	Asn	Ser	Gly	Thr	Pro	Lys	
77						260				265					270		
78	gac	cac	gac	tcc	cct	gag	aac	ggt	gcg	gac	agc	ttc	gag	agc	tca	gac	1161
79	Asp	His	Asp	Ser	Pro	Glu	Asn	Gly	Ala	Asp	Ser	Phe	Glu	Ser	Ser	Asp	
80						275				280					285		290
81	tcc	ctc	ctc	cag	tcc	ttg	aac	agc	cag	tgc	tcc	ttg	ctg	gat	gtg	caa	1209
82	Ser	Leu	Leu	Gln	Ser	Trp	Asn	Ser	Gln	Ser	Ser	Leu	Leu	Asp	Val	Gln	
83						295				300					305		
84	cggtt	cct	tcc	ttc	gag	agc	tcc	gaa	gat	gac	tgc	agc	cag	tct	ctc	1257	
85	Arg	Val	Pro	Ser	Phe	Glu	Ser	Phe	Glu	Asp	Asp	Cys	Ser	Gln	Ser	Leu	
86						310				315					320		
87	tgc	ctc	aat	aag	cca	acc	atg	tct	ttc	aag	gat	tac	atc	caa	gag	agg	1305
88	Cys	Leu	Asn	Lys	Pro	Thr	Met	Ser	Phe	Lys	Asp	Tyr	Ile	Gln	Glu	Arg	
89						325				330					335		
90	agt	gac	cca	gtg	gag	caa	ggc	aaa	cca	gtt	ata	cct	gca	gct	gtg	ctg	1353
91	Ser	Asp	Pro	Val	Glu	Gln	Gly	Lys	Pro	Val	Ile	Pro	Ala	Ala	Val	Leu	
92						340				345					350		
93	gcc	ggc	tcc	aca	gga	agt	gga	cct	att	cag	ctg	tgg	cag	ttt	ctc	ctg	1401
94	Ala	Gly	Phe	Thr	Gly	Ser	Gly	Pro	Ile	Gln	Leu	Trp	Gln	Phe	Leu	Leu	
95						355				360					365		370
96	gag	ctg	cta	tca	gac	aaa	tcc	tgc	cag	tca	ttc	atc	agc	tgg	act	gga	1449
97	Glu	Leu	Leu	Ser	Asp	Lys	Ser	Cys	Gln	Ser	Phe	Ile	Ser	Trp	Thr	Gly	

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98	375	380	385	
99	gac gga tgg gag ttt aag ctc gcc gac ccc gat gag gtg gcc cgc cgg			1497
100	Asp Gly Trp Glu Phe Lys Leu Ala Asp Pro Asp Glu Val Ala Arg Arg			
101	390	395	400	
102	tgg gga aag agg aaa aat aag ccc aag atg aac tac gag aag ctg agc			1545
103	Trp Gly Lys Arg Lys Asn Lys Pro Lys Met Asn Tyr Glu Lys Leu Ser			
104	405	410	415	
105	cgg ggc tta cgc tac tat tac gac aag aac atc atc cac aag acg tcg			1593
106	Arg Gly Leu Arg Tyr Tyr Asp Lys Asn Ile Ile His Lys Thr Ser			
107	420	425	430	
108	ggg aag cgc tac gtg tac cgc ttc gtg tgc gac ctc cag aac ttg ctg			1641
109	Gly Lys Arg Tyr Val Tyr Arg Phe Val Cys Asp Leu Gln Asn Leu Leu			
110	435	440	445	450
111	ggg ttc acg ccc gag gaa ctg cac gcc atc ctg ggc gtc cag ccc gac			1689
112	Gly Phe Thr Pro Glu Glu Leu His Ala Ile Leu Gly Val Gln Pro Asp			
113	455	460	465	
114	acg gag gac tgaggtcgcc gggaccaccc tgagccggcc ccaggctcg			1738
115	Thr Glu Asp			
117	ggactgagtg ggaagccat cctgaccagc tgcctccgag gacccaggaa aggcaggatt			1798
118	gaaaatgtcc aggaaagtgg ccaagaagca gtggccttat tgcatcccaa accacgcctc			1858
119	ttgaccaggc tgcctccctt gtggcagcaa cggcacagct aattctactc acagtgcctt			1918
120	taagtgaaaa tggtcgagaa agaggcaccc ggaagccgtc ctggcgcctg gcagtcgtg			1978
121	ggacgggatg gttctggctg tttgagattc tcaaaggagc gagcatgtcg tggacacaca			2038
122	cagactattt ttagattttc ttttgccttt tgcaaccagg aacagcaaat gcaaaaactc			2098
123	tttgagaggg taggagggtg ggaaggaaac aaccatgtca tttcagaagt tagttgtat			2158
124	atattataat aatctataa ttgttctcag aatcccttaa cagttgtatt taacagaaat			2218
125	tgtatattgt aatttaaat aattatataa ctgtatttga aataagaatt c			2269
127	<210> SEQ ID NO: 2			
128	<211> LENGTH: 469			
129	<212> TYPE: PRT			
130	<213> ORGANISM: Homo sapiens			
131	<400> SEQUENCE: 2			
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134	Asn Ser Tyr Arg Gly Thr Leu Lys Arg Gln Pro Ala Phe Asp Thr Phe			
135	20	25	30	
136	Asp Gly Ser Leu Phe Ala Val Phe Pro Ser Leu Asn Glu Glu Gln Thr			
137	35	40	45	
138	Leu Gln Glu Val Pro Thr Gly Leu Asp Ser Ile Ser His Asp Ser Ala			
139	50	55	60	
140	Asn Cys Glu Leu Pro Leu Leu Thr Pro Cys Ser Lys Ala Val Met Ser			
141	65	70	75	80
142	Gln Ala Leu Lys Ala Thr Phe Ser Gly Phe Lys Lys Glu Gln Arg Arg			
143	85	90	95	
144	Leu Gly Ile Pro Lys Asn Pro Trp Leu Trp Ser Glu Gln Gln Val Cys			
145	100	105	110	
146	Gln Trp Leu Leu Trp Ala Thr Asn Glu Phe Ser Leu Val Asn Val Asn			
147	115	120	125	
148	Leu Gln Arg Phe Gly Met Asn Gly Gln Met Leu Cys Asn Leu Gly Lys			

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149	130	135	140
150	Glu Arg Phe Leu Glu Leu Ala Pro Asp Phe Val Gly Asp Ile Leu Trp		
151	145	150	155
152	Glu His Leu Glu Gln Met Ile Lys Glu Asn Gln Glu Lys Thr Glu Asp		160
153	165	170	175
154	Gln Tyr Glu Glu Asn Ser His Leu Thr Ser Val Pro His Trp Ile Asn		
155	180	185	190
156	Ser Asn Thr Leu Gly Phe Gly Thr Glu Gln Ala Pro Tyr Gly Met Gln		
157	195	200	205
158	Thr Gln Asn Tyr Pro Lys Gly Gly Leu Leu Asp Ser Met Cys Pro Ala		
159	210	215	220
160	Ser Thr Pro Ser Val Leu Ser Ser Glu Gln Glu Phe Gln Met Phe Pro		
161	225	230	235
162	240	Lys Ser Arg Leu Ser Ser Val Ser Val Thr Tyr Cys Ser Val Ser Gln	
163	245	250	255
164	Asp Phe Pro Gly Ser Asn Leu Asn Leu Leu Thr Asn Asn Ser Gly Thr		
165	260	265	270
166	Pro Lys Asp His Asp Ser Pro Glu Asn Gly Ala Asp Ser Phe Glu Ser		
167	275	280	285
168	Ser Asp Ser Leu Leu Gln Ser Trp Asn Ser Gln Ser Ser Leu Leu Asp		
169	290	295	300
170	Val Gln Arg Val Pro Ser Phe Glu Ser Phe Glu Asp Asp Cys Ser Gln		
171	305	310	315
172	320	Ser Leu Cys Leu Asn Lys Pro Thr Met Ser Phe Lys Asp Tyr Ile Gln	
173	325	330	335
174	Glu Arg Ser Asp Pro Val Glu Gln Gly Lys Pro Val Ile Pro Ala Ala		
175	340	345	350
176	350	355	360
177	365	Val Leu Ala Gly Phe Thr Gly Ser Gly Pro Ile Gln Leu Trp Gln Phe	
178	370	375	380
179	380	Leu Leu Glu Leu Leu Ser Asp Lys Ser Cys Gln Ser Phe Ile Ser Trp	
180	385	390	395
181	400	Thr Gly Asp Gly Trp Glu Phe Lys Leu Ala Asp Pro Asp Glu Val Ala	
182	405	410	415
183	415	Arg Arg Trp Gly Lys Arg Lys Asn Lys Pro Lys Met Asn Tyr Glu Lys	
184	420	425	430
185	430	Leu Ser Arg Gly Leu Arg Tyr Tyr Asp Lys Asn Ile Ile His Lys	
186	435	440	445
187	445	Thr Ser Gly Lys Arg Tyr Val Tyr Arg Phe Val Cys Asp Leu Gln Asn	
188	450	455	460
189	460	Leu Leu Gly Phe Thr Pro Glu Glu Leu His Ala Ile Leu Gly Val Gln	
190	465	Pro Asp Thr Glu Asp	
191	465	<210> SEQ ID NO: 3	
192	465	<211> LENGTH: 84	
193	465	<212> TYPE: PRT	
194	465	<213> ORGANISM: Homo sapiens	
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196	465	Ser Gly Pro Ile Gln Leu Trp Gln Phe Leu Leu Glu Leu Thr Asp	

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199 1 5 10 15
 200 Lys Ser Cys Gln Ser Phe Ile Ser Trp Thr Gly Asp Gly Trp Glu Phe
 201 20 25 30
 202 Lys Leu Ser Asp Pro Asp Glu Val Ala Arg Arg Trp Gly Lys Arg Lys
 203 35 40 45
 204 Asn Lys Pro Lys Met Asn Tyr Glu Lys Leu Ser Arg Gly Leu Arg Tyr
 205 50 55 60
 206 Tyr Tyr Asp Lys Asn Ile Ile His Lys Thr Ala Gly Lys Arg Tyr Val
 207 65 70 75 80
 208 Tyr Arg Phe Val
 210 <210> SEQ ID NO: 4
 211 <211> LENGTH: 84
 212 <212> TYPE: PRT
 213 <213> ORGANISM: Mus musculus
 214 <400> SEQUENCE: 4
 215 Ser Gly Pro Ile Gln Leu Trp Gln Phe Leu Leu Glu Leu Leu Thr Asp
 216 1 5 10 15
 217 Lys Ser Cys Gln Ser Phe Ile Ser Trp Thr Gly Asp Gly Trp Glu Phe
 218 20 25 30
 219 Lys Leu Ser Asp Pro Asp Glu Val Ala Arg Arg Trp Gly Lys Arg Lys
 220 35 40 45
 221 Asn Lys Pro Lys Met Asn Tyr Glu Lys Leu Ser Arg Gly Leu Arg Tyr
 222 50 55 60
 223 Tyr Tyr Asp Lys Asn Ile Ile His Lys Thr Ala Gly Lys Arg Tyr Val
 224 65 70 75 80
 225 Tyr Arg Phe Val
 227 <210> SEQ ID NO: 5
 228 <211> LENGTH: 84
 229 <212> TYPE: PRT
 230 <213> ORGANISM: Gallus gallus
 231 <400> SEQUENCE: 5
 232 Ser Gly Pro Ile Gln Leu Trp Gln Phe Leu Leu Glu Leu Leu Thr Asp
 233 1 5 10 15
 234 Lys Ser Cys Gln Ser Phe Ile Ser Trp Thr Gly Asp Gly Trp Glu Phe
 235 20 25 30
 236 Lys Leu Ser Asp Pro Asp Glu Val Ala Arg Arg Trp Gly Lys Arg Lys
 237 35 40 45
 238 Asn Lys Pro Lys Met Asn Tyr Glu Lys Leu Ser Arg Gly Leu Arg Tyr
 239 50 55 60
 240 Tyr Tyr Asp Lys Asn Ile Ile His Lys Thr Ala Gly Lys Arg Tyr Val
 241 65 70 75 80
 242 Tyr Arg Phe Val
 244 <210> SEQ ID NO: 6
 245 <211> LENGTH: 84
 246 <212> TYPE: PRT
 247 <213> ORGANISM: Xenopus laevis
 248 <400> SEQUENCE: 6
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 250 1 5 10 15

VERIFICATION SUMMARY

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